

Meyers et al - SEQ ID NO: 3

RESULT 4

US-09-800-971-3

; Sequence 3, Application US/09800971

; Patent No. 6534301

; GENERAL INFORMATION:

; APPLICANT: Rachel A. Meyers

; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C

; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

; FILE REFERENCE: 10448-023001

; CURRENT APPLICATION NUMBER: US/09/800,971

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/187,453

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: 60/188,032

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2211

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-800-971-3

Query Match 8.3%; Score 301.8; DB 3; Length 2211;

Best Local Similarity 54.0%; Pred. No. 1.2e-51;

Matches 743; Conservative 0; Mismatches 607; Indels 27; Gaps 5;

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Qy      111 GGTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGG 170
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Db      12  GGAGGACGAGGACGTGCGCGCCATGCTGCGGGGCTCCCGGCTCCGCAAGATCCGCTCGCG 71

Qy      171 CTCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCAC-----CGCTCCTGCATCCG 224
          |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      72  CACGTGGCAAGGAGCGGCTGTACCGGCTGCAGGAGGACGGCCTGAGCGTGTGGTTCCA 131

Qy      225 CTGGAGGCCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGT 284
          || |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      132 GCGGCGCATCCCGCGTGCGCCATCGCAGCACATCTTCTTCGTGCAGCACATCGAGGCGGT 191

Qy      285 GAGTGAGGGGCGGCAGTCGGAGGTCTTCCAGCGCTACCTGACGGCAGCTTCGACCCCAA 344
          |  |||||  |  |||||  ||||  |  |  |||||  |  |  ||  |||||  |
Db      192 CCGCGAGGGCCACCAAGTCCGAGGGCCTGCGGCGCTTC---GGGGGTGCCTTCGCGCCAGC 248

Qy      345 CTGCTGCTTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAG 404
          |||||  ||  ||||  |  |  ||  ||||  ||  |||||  ||||  |  ||
Db      249 GCGCTGCCTCACCATCGCCTTCAAGGGCCGCCGCAAGAACCTGGACCTGGCGGCGCCAC 308

Qy      405 CAGCGAGGTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGA 464
          ||||  ||||  |||||  ||  |||  |  |  |||  ||  ||  ||  ||
Db      309 GGCTGAGGAAGCGCAGCGCTGGGTGCGCGTCTGACCAAGCTCCGCGCGCGCCTGGACGC 368

Qy      465 CGAGGACAGCCTGGCTCGCCGCCAGCGCACCAGGGACCAAGTGGCTGAAGCAGACGTTTGA 524
          |  |  |  |  |  ||  |  |||||  |||  |  |  |  |  |
Db      369 CATGAGCCAGCGCGAGCGGCT-----AGACCACTGGATCCACTCCTATCTGCA 416

Qy      525 CGAGGCCGACAAGAACGGGGATGGCAGCCTGAGCATTGCGGAGGTCCTGCAGCTGCTGCA 584
          |  |||  |||  |||  |||  |||  |||||  |  |||  ||  |||||
Db      417 CCGGGCTGACTCCAACCAGGACAGCAAGATGAGCTTCAAGGAGATCAAGAGCCTGCTGAG 476

Qy      585 CAAGCTCAACGTGAACCTGCCCGGCAGAGGGTGAAGCAGATGTTTCAGGGAAGCGGACAC 644
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Db	477	AATGGTCAACGTGGACATGAACGACATGTACGCCTACCTCCTCTTCAAGGAGTGTGAC--	534
Qy	645	GGATGACCAACCAAGGGACGCTGGGTTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTC	704
Db	535	-CACTCCAACAACGACCGTCTAGAGGGGGCTGAGATCGAGGAGTTCCTGCGGCGGCTGCT	593
Qy	705	CACCCGCCGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGA	764
Db	594	GAAGCGGCCGGAGCTGGAGGAGATCTTCCATCAGTACTCGGGCGAGGACCGCGTGTGAG	653
Qy	765	TGCCGCCAGCCTGCAGCGCTTCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGA	824
Db	654	TGCCCCCTGAGCTGCTGGAGTTCTCT---GGAGGACCAGGGCGAGGAGGGCGCCACACTGGC	710
Qy	825	GAGCTGCCAGGACATCATCGAGCAGTTTGAGCCATGCCCAGAAAACAAGATAAGGGGGCT	884
Db	711	CCGCGCCAGCAGCTCATTAGACCTATGAGCTCAACGAGACAGCCAAGCAGCATGAGCT	770
Qy	885	GCTGGGCATTGATGGCTTACCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCC	944
Db	771	GATGACACTGGATGGCTTCATGATGTACCTGTTGTCGCCGAGGGGGCTGCCTTGGACAA	830
Qy	945	TGAGCACCACCATGTGCACCAGGACATGACGCAGCCGCTGAGCCACTACTTCATCACCTC	1004
Db	831	CACCCACACGTGTGTGTTCCAGGACATGAACCAGCCCCCTGCCCACTACTTCATCTCTTC	890
Qy	1005	GTCCCAACAACCTACCTCGTGGGTGACCAGCTCATGTCCAGTCACGGGTGGACATGTA	1064
Db	891	CTCCCAACAACCTATCTGACTGACTCCAGATCGGGGGGGCCAGCAGCACCGAGGCCTA	950
Qy	1065	TGCTTGGGTCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCCGA	1124
Db	951	TGTTAGGGCCTTTGCCAGGGATGCCGCTGCGTGGAGCTGGACTGCTGGGAGGGGCCAGG	1010
Qy	1125	CGGGGAGCCCATTTGTGCACCATGGCTACACTCTGACTTCCAAGATCCTCTTCAAAGACGT	1184
Db	1011	AGGGGAGCCCGTCATCTATCATGGCCATACCCTCACCTCCAAGATTCTCTTCCGGGACGT	1070
Qy	1185	CATTGAAACCATCAACAAATATGCTTCATCAAGAAAGAGTACCCAGTGATCCTGTCCAT	1244
Db	1071	GGTCCAAGCCGTGCGCGACCATGCTTCACGCTGTCCCCTTACCCTGTATCCTATCCCT	1130
Qy	1245	CGAAAACCACTGCAGTGTATCCAGCAGAAGAAAATGGCCCACTATCTGACTGACATCCT	1304
Db	1131	GGAGAACCACTGCGGGCTGGAGCAGCAGGCTGCCATGGCCGCCACCTCTGCACCATCCT	1190
Qy	1305	TGGGGACAAGCTGGACCTGTCATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCC	1364
Db	1191	GGGGGACATGCTGGTGACACAGGCGCTGGACTCCCCAAATCCCGAGGAGCTGCCATCCCC	1250
Qy	1365	ACAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCAGCCAACATCAGCGA	1424
Db	1251	AGAGCAGCTGAAGGGCCGGGTCTGGTGAAGGGGAAGAAGCTGCCCGCTGCTCGGAGCGA	1310
Qy	1425	GGATGCGGAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGA	1481
Db	1311	GGATGGCCGGGCTCTGTGCGATCGGGAGGAGGAGGAGGAGGATGACGAGGAGGAAGA	1367

Meyer et al - SEQ ID NO: 2

RESULT 4

US-09-800-971-9

; Sequence 9, Application US/09800971

; Patent No. 6534301

; GENERAL INFORMATION:

; APPLICANT: Rachel A. Meyers

; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C

; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

; FILE REFERENCE: 10448-023001

; CURRENT APPLICATION NUMBER: US/09/800,971

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/187,453

; PRIOR FILING DATE: 2000-03-07

; PRIOR APPLICATION NUMBER: 60/188,032

; PRIOR FILING DATE: 2000-03-09

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 119

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: consensus sequence

US-09-800-971-9

Query Match 1.0%; Score 12; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 694 FWNAGCQMVALN 705

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Db 77 FWNAGCQMVALN 88

Seq ID No. 1

RESULT 4

US-09-800-971-3

; Sequence 3, Application US/09800971

; Patent No. 6534301

; GENERAL INFORMATION:

; APPLICANT: Rachel A. Meyers

; TITLE OF INVENTION: 16835, A NOVEL HUMAN PHOSPHOLIPASE C

; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

; FILE REFERENCE: 10448-023001

; CURRENT APPLICATION NUMBER: US/09/800,971

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/187,453

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; PRIOR APPLICATION NUMBER: 60/188,032

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; TYPE: DNA

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US-09-800-971-3

Query Match 6.5%; Score 301.8; DB 3; Length 2211;

Best Local Similarity 54.0%; Pred. No. 4.3e-51;

Matches 743; Conservative 0; Mismatches 607; Indels 27; Gaps 5;

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Qy      545 GGTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGG 604
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Db      12  GGAGGACGAGGACGTGCGCGCCATGCTGCGGGGCTCCCGGCTCCGCAAGATCCGCTCGCG 71

Qy      605 CTCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCAC-----CGCTCCTGCATCCG 658
      | |  |  |  ||  ||  ||||  |||  |||  ||  ||  ||  ||
Db      72  CACGTGGCACAAGGAGCGGCTGTACCGGCTGCAGGAGGACGGCCTGAGCGTGTGTTCCA 131

Qy      659 CTGGAGGCCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGT 718
      || |  |  |||  |  ||  |  ||  ||  |||  ||  |  |||  |||  |||
Db      132 GCGGCGCATCCCGCGTGCGCCATCGCAGCACATCTTCTTCGTGCAGCACATCGAGGCGGT 191

Qy      719 GAGTGAGGGGCGGCAGTCGGAGGTCTTCCAGCGCTACCCTGACGGCAGCTTCGACCCCAA 778
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Db      192 CCGCGAGGGCCACCAGTCCGAGGGCCTGCGGCGCTTC---GGGGGTGCCTTCGCGCCAGC 248

Qy      779 CTGCTGCTTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAG 838
      |||||  |||  ||||  |  |  ||  ||||  ||  |||||  ||||  |  |||
Db      249 GCGCTGCCTCACCATCGCCTTCAAGGGCCGCCGCAAGAACCTGGACCTGGCGGCGCCAC 308

Qy      839 CAGCGAGGTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGA 898
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Db      309 GGCTGAGGAAGCGCAGCGCTGGGTGCGCGTCTGACCAAGCTCCGCGCGCGCCTGGACGC 368

Qy      899 CGAGGACAGCCTGGCTCGCCGCCAGCGCACCAGGGACCAGTGGCTGAAGCAGACGTTTGA 958
      |  |  |  |  |  ||  |  |||||  |||  |  |  |  |  |
Db      369 CATGAGCCAGCGCGAGCGGCT-----AGACCACTGGATCCACTCCTATCTGCA 416

Qy      959 CGAGGCCGACAAGAACGGGGATGGCAGCCTGAGCATTGCGGAGGTCCTGCAGCTGCTGCA 1018
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Db      417 CCGGGTGACTCCAACCAGGACAGCAAGATGAGCTTCAAGGAGATCAAGAGCCTGCTGAG 476

Qy      1019 CAAGCTCAACGTGAACCTGCCCGGCAGAGGGTGAAGCAGATGTTTCAGGGAAGCGGACAC 1078
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Db	477	AATGGTCAACGTGGACATGAACGACATGTACGCCTACCTCCTCTTCAAGGAGTGTGAC--	534
Qy	1079	GGATGACCACCAAGGGACGCTGGGTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTC	1138
Db	535	-CACTCCAACAACGACCGTCTAGAGGGGGCTGAGATCGAGGAGTTCCTGCGGCGGCTGCT	593
Qy	1139	CACCCGCCGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGA	1198
Db	594	GAAGCGGCCGGAGCTGGAGGAGATCTTCATCAGTACTCGGGCGAGGACCGCGTGTGAG	653
Qy	1199	TGCCGCCAGCCTGCAGCGCTTCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGA	1258
Db	654	TGCCCCCTGAGCTGCTGGAGTTCCT---GGAGGACCAGGGCGAGGAGGGCGCCACACTGGC	710
Qy	1259	GAGCTGCCAGGACATCATCGAGCAGTTTGAGCCATGCCAGAAAACAAGAGTAAGGGGCT	1318
Db	711	CCGCGCCAGCAGCTCATTAGACCTATGAGCTCAACGAGACAGCCAAGCAGCATGAGCT	770
Qy	1319	GCTGGGCATTGATGGCTTCACCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCC	1378
Db	771	GATGACACTGGATGGCTTCATGATGTACCTGTTGTCGCCGAGGGGGCTGCCTTGGACAA	830
Qy	1379	TGAGCACCACCATGTGCACCAGGACATGACGCAGCCGCTGAGCCACTACTTCATCACCTC	1438
Db	831	CACCCACACGTGTGTGTTCAGGACATGAACCAGCCCTTGCCCCACTACTTCATCTCTTC	890
Qy	1439	GTCCCACAACACCTACCTCGTGGGTGACCAGCTCATGTCCAGTACCGGGTGGACATGTA	1498
Db	891	CTCCCACAACACCTATCTGACTGACTCCAGATCGGGGGGCCAGCAGCACCGAGGCCTA	950
Qy	1499	TGCTTGGGTCTGCAGGCTGGCTGCCGCTGCGTGAGGTGGACTGCTGGGATGGGCCCGA	1558
Db	951	TGTTAGGGCCTTTGCCAGGGATGCCGCTGCGTGAGCTGGACTGCTGGGAGGGGCCAGG	1010
Qy	1559	CGGGGAGCCCATTTGTGCACCATGGCTACACTCTGACTTCCAAGATCCTCTTCAAAGACGT	1618
Db	1011	AGGGGAGCCCGTCATCTATCATGGCCATACCTCACCTCCAAGATTCTCTTCGGGACGT	1070
Qy	1619	CATTGAAACCATCAACAAATATGCCTTCATCAAGAAATGAGTACCCAGTGATCCTGTCCAT	1678
Db	1071	GGTCCAAGCCGTGCGCGACCATGCCTTCACGCTGTCCCTTACCTGTATCCTATCCCT	1130
Qy	1679	CGAAAACCACTGCAGTGTTCATCCAGCAGAAGAAAATGGCCAGTATCTGACTGACATCCT	1738
Db	1131	GGAGAACCACTGCGGGCTGGAGCAGCAGGCTGCCATGGCCGCCACCTCTGCACCATCCT	1190
Qy	1739	TGGGGACAAGCTGGACCTGTTCATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCC	1798
Db	1191	GGGGGACATGCTGGTGACACAGGCGCTGGACTCCCCAAATCCCGAGGAGCTGCCATCCCC	1250
Qy	1799	ACAGATGCTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCAGCCAACATCAGCGA	1858
Db	1251	AGAGCAGCTGAAGGGCCGGGTCTGGTGAAGGGAAAGAAGCTGCCGCTGCTCGGAGCGA	1310
Qy	1859	GGATGCGGAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGA	1915
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seq no. SEQ ID NO: 3

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DEFINITION Homo sapiens mRNA for KIAA0450 protein, partial cds.
ACCESSION AB007919
VERSION AB007919.2 GI:58257651
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Seki,N., Ohira,M., Nagase,T., Ishikawa,K., Miyajima,N.,
Nakajima,D., Nomura,N. and Ohara,O.
TITLE Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain
JOURNAL DNA Res. 4 (5), 345-349 (1997)
PUBMED 9455484
REFERENCE 2 (bases 1 to 5450)
AUTHORS Ohara,O.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Kazusa-kamatari 2-6-7, Kisarazu,
Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,
Tel:81-438-52-3913, Fax:81-438-52-3914)
COMMENT On Jan 27, 2005 this sequence version replaced gi:3413861.
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/clone="hj05822"
/tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
/note="This sequence was replaced that of hg00217 cDNA as
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/gene="KIAA0450"
CDS <1. .3551
/gene="KIAA0450"
/codon_start=3
/product="KIAA0450 protein"
/protein_id="BAA32295.3"
/db_xref="GI:58257652"
/translation="RAGAAGQVRVGLRSAWALRAGCPCSGWGSAGGQHRARCPSGRA
GNWDWHPPAMEEPGPPGGLSQDQVERCMGAMQEGMQMVKLRGGSKGLVRFYILDEHRS
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LVSTSSEVARTWVTGLRYLMAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIG
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RVLDGPGPAGMAATCMKCVVSGCAGVNTGGLQGRSERPPSPGPASRQAAIRQQPRARADS
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ORIGIN

Query Match 92.1%; Score 3339.2; DB 5; Length 5450;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3347; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy	172	TCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG	231
Db	264	TCCAAGGGCCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG	323
Qy	232	CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG	291
Db	324	CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG	383
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Db	384	GGGCGGCAGTCGGAGGTCTTCAGCGCTACCCTGACGGCAGCTTCGACCCCAACTGCTGC	443
Qy	352	TTCAGCATCTACCACGGCAGCCACC CGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	411
Db	444	TTCAGCATCTACCACGGCAGCCACC CGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	503
Qy	412	GTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	471
Db	504	GTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	563
Qy	472	AGCCTGGCTCGCCGCCAGCGCACCCAGGGACCAGTGGCTGAAGCAGACGTTTGACGAGGCC	531
Db	564	AGCCTGGCTCGCCGCCAGCGCACCCAGGGACCAGTGGCTGAAGCAGACGTTTGACGAGGCC	623
Qy	532	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTTGACGCTGCTGCACAAGCTC	591
Db	624	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTTGACGCTGCTGCACAAGCTC	683
Qy	592	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTT CAGGGAAGCGGACACGGATGAC	651
Db	684	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTT CAGGGAAGCGGACACGGATGAC	743
Qy	652	CACCAAGGGACGCTGGGTTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGC	711
Db	744	CACCAAGGGACGCTGGGTTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGC	803
Qy	712	CGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCC	771
Db	804	CGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCC	863
Qy	772	AGCCTGCAGCGCTTCCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGAGAGCTGC	831
Db	864	AGCCTGCAGCGCTTCCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGAGAGCTGC	923
Qy	832	CAGGACATCATCGAGCAGTTT GAGCCATGCCCAGAAAA CAAGAGTAAGGGGCTGCTGGGC	891

Db	924	 CAGGACATCATCGAGCAGTTTGGAGCCATGCCAGAAAACAAGAGTAAGGGGCTGCTGGGC	983
Qy	892	ATTGATGGCTTCACCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCAC	951
Db	984	 ATTGATGGCTTCACCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCAC	1043
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Db	1044	 CACCATGTGCACCAGGACATGACGAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAC	1103
Qy	1012	AACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGG	1071
Db	1104	 AACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGG	1163
Qy	1072	GTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCCCGACGGGGAG	1131
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Qy	1312	AAGCTGGACCTGTATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCACAGATG	1371
Db	1404	 AAGCTGGACCTGTATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCACAGATG	1463
Qy	1372	CTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCAGCCAACATCAGCGAGGATGCG	1431
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Qy	1432	GAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTC	1491
Db	1524	 GAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTC	1583
Qy	1492	CTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAAACTG	1551
Db	1584	 CTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAAACTG	1643
Qy	1552	GATTCCTCATCAAAGAGTCGAAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTC	1611
Db	1644	 GATTCCTCATCAAAGAGTCGAAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTC	1703
Qy	1612	TCCACACTGTCCCATCTGGAAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAG	1671
Db	1704	 TCCACACTGTCCCATCTGGAAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAG	1763
Qy	1672	TCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCTCGTCTGCGGGAAGCTTCTCC	1731
Db	1764	 TCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCTCGTCTGCGGGAAGCTTCTCC	1823
Qy	1732	AGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGCCAGCGTGGAGGAGGGAGATGAG	1791

Db	1824	AGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGGAGATGAG	1883
Qy	1792	GGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAG	1851
Db	1884	GGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAG	1943
Qy	1852	CTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATA	1911
Db	1944	CTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATA	2003
Qy	1912	GAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACCAG	1971
Db	2004	GAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACCAG	2063
Qy	1972	ATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCCCGCATC	2031
Db	2064	ATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCCCGCATC	2123
Qy	2032	TACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCC	2091
Db	2124	TACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCC	2183
Qy	2092	GGTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGA	2151
Db	2184	GGTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGA	2243
Qy	2152	GCCAAGTTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAG	2211
Db	2244	GCCAAGTTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAG	2303
Qy	2212	GGCGTGTTCAAACCCCAACTCGGAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTG	2271
Db	2304	GGCGTGTTCAAACCCCAACTCGGAGGACCCCTGCCCGGGCAGCTCAAGAAGCAGCTGGTG	2363
Qy	2272	CTCCGGATCATCAGTGGCCAGCAGCTTCCAAGCCGCGGACTCCATGCTGGGGGACCGT	2331
Db	2364	CTCCGGATCATCAGTGGCCAGCAGCTTCCAAGCCGCGGACTCCATGCTGGGGGACCGT	2423
Qy	2332	GGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGC	2391
Db	2424	GGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGC	2483
Qy	2392	AGGGAGCAGACCCGCGTGGTGGACGACAACGGGTTCACCCACCTGGGAGGAGACCCTG	2451
Db	2484	AGGGAGCAGACCCGCGTGGTGGACGACAACGGGTTCACCCACCTGGGAGGAGACCCTG	2543
Qy	2452	GTTTTTCATGGTGCACATGCCGAGATCGCGCTGGTCCGCTCCTCGTCTGGGACCACGAT	2511
Db	2544	GTTTTTCATGGTGCACATGCCGAGATCGCGCTGGTCCGCTCCTCGTCTGGGACCACGAT	2603
Qy	2512	CCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGC	2571
Db	2604	CCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGC	2663
Qy	2572	TACAGACACGTGTACCTAGAAGGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTC	2631
Db	2664	TACAGACACGTGTACCTAGAAGGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTC	2723
Qy	2632	AGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGC	2691
Db	2724	AGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGC	2783

Qy	2692	CCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCGTT	2751
Db	2784	CCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCGTT	2843
Qy	2752	AGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGC	2811
Db	2844	AGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGC	2903
Qy	2812	AGGGGCTTCCCGAGCTGGTCCTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGAC	2871
Db	2904	AGGGGCTTCCCGAGCTGGTCCTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGAC	2963
Qy	2872	GATGTGGTGCCCCCGGGGCCGGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGGCCCGGC	2931
Db	2964	GATGTGGTGCCCCCGGGGCCGGACCTGCTCCGGAAGCCCCAGCCCAGGAGGGGCCCGGC	3023
Qy	2932	AGCGGCAGCCCCGAGGTAAGGCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTG	2991
Db	3024	AGCGGCAGCCCCGAGGTAAGGCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTG	3083
Qy	2992	CGGCCCCCGCGTGTCTCTGGACGGCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAG	3051
Db	3084	CGGCCCCCGCGTGTCTCTGGACGGCCCGGGCCTGCTGGGATGGCCGCCACATGCATGAAG	3143
Qy	3052	TGTGTGGTGGGATCCTGCGCCGGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCC	3111
Db	3144	TGTGTGGTGGGATCCTGCGCCGGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCC	3203
Qy	3112	AGCCCGGGGCTGCAAGCAGGCAGGCAGCCATTTCGCCAGCAGCCCCGGGCCCGGGCTGAC	3171
Db	3204	AGCCCGGGGCTGCAAGCAGGCAGGCAGCCATTTCGCCAGCAGCCCCGGGCCCGGGCTGAC	3263
Qy	3172	TCACTGGGGGCCCCCTGCTGTGGCCTGGACCTCACGCTATCCCGGGGAGAAGCAGAGAG	3231
Db	3264	TCACTGGGGGCCCCCTGCTGTGGCCTGGACCTCACGCTATCCCGGGGAGAAGCAGAGAG	3323
Qy	3232	GCCCCCAAGGGTCCTGGGGCCTGGAGGCAGGGTCAGGCGGTAGCGGCTCCATGTCCTCG	3291
Db	3324	GCCCCCAAGGGTCCTGGGGCCTGGAGGCAGGGTCAGGCGGTAGCGGCTCCATGTCCTCG	3383
Qy	3292	GACTCCAGCAGCCCAGACAGCCCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGT	3351
Db	3384	GACTCCAGCAGCCCAGACAGCCCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGT	3443
Qy	3352	GCCTGCAGGCAACCGGGGGCCCTGCAGGGAGAGATGAGTGCCTTGTTTGCTCAAAAGCTG	3411
Db	3444	GCCTGCAGGCAACCGGGGGCCCTGCAGGGAGAGATGAGTGCCTTGTTTGCTCAAAAGCTG	3503
Qy	3412	GAGGAGATCAGGAGTAAATCCCCATGTTCTCCGCCGGTAAGCCCCCTTGCCCTGCGTG	3471
Db	3504	GAGGAGATCAGGAGTAAATCCCCATGTTCTCCGCCGGTAGGAACTGAGAGCGGCGAGTG	3563

Seki et al - SZ2 ID 10-2

RESULT 2

PLCL4_HUMAN

ID PLCL4_HUMAN STANDARD; PRT; 1182 AA.
AC O75038;
DT 21-FEB-2001, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2005, sequence version 2.
DT 07-FEB-2006, entry version 24.
DE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase-like 4
DE (EC 3.1.4.11) (Phosphoinositide phospholipase C-like 4) (Phospholipase
DE C-like 4) (Fragment).
GN Name=PLCL4; Synonyms=KIAA0450;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Brain;
RX MEDLINE=98116662; PubMed=9455484; DOI=10.1093/dnares/4.5.345;
RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
RA Nomura N., Ohara O.;
RT "Characterization of cDNA clones in size-fractionated cDNA libraries
RT from human brain.";
RL DNA Res. 4:345-349(1997).
RN [2]
RP SEQUENCE REVISION.
RA Seki N., Ohira M., Nagase T., Ishikawa K., Miyajima N., Nakajima D.,
RA Nomura N., Ohara O.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: The production of the second messenger molecules
CC diacylglycerol (DAG) and inositol 1,4,5-trisphosphate (IP3) is
CC mediated by activated phosphatidylinositol-specific phospholipase
CC C enzymes (By similarity).
CC -!- CATALYTIC ACTIVITY: 1-phosphatidyl-1D-myo-inositol 4,5-
CC bisphosphate + H(2)O = 1D-myo-inositol 1,4,5-trisphosphate +
CC diacylglycerol.
CC -!- COFACTOR: Calcium (By similarity).
CC -!- SIMILARITY: Contains 1 C2 domain.
CC -!- SIMILARITY: Contains 2 EF-hand domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 1 PI-PLC X-box domain.
CC -!- SIMILARITY: Contains 1 PI-PLC Y-box domain.
CC -----
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CC -----
DR EMBL; AB007919; BAA32295.3; -; mRNA.
DR HGNC; HGNC:29037; PLCL4.
DR InterPro; IPR000008; C2.
DR InterPro; IPR011992; EF-Hand_type.
DR InterPro; IPR002048; EF_hand_Ca_bd.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH_type.
DR InterPro; IPR001192; PI-PLC.
DR InterPro; IPR000909; PI-PLC_X.
DR InterPro; IPR001711; PI-PLC_Y.
DR Pfam; PF00168; C2; 1.
DR Pfam; PF00036; efhand; 1.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00388; PI-PLC-X; 1.

DR Pfam; PF00387; PI-PLC-Y; 1.
 DR PRINTS; PR00360; C2DOMAIN.
 DR PRINTS; PR00390; PHPHLIPASEC.
 DR ProDom; PD000012; EF-hand; 1.
 DR ProDom; PD001202; PI_PLC_Y; 2.
 DR SMART; SM00239; C2; 1.
 DR SMART; SM00054; EFh; 2.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00148; PLCXc; 1.
 DR SMART; SM00149; PLCYc; 1.
 DR PROSITE; PS50004; C2_DOMAIN; 1.
 DR PROSITE; PS00018; EF_HAND_1; 1.
 DR PROSITE; PS50222; EF_HAND_2; 2.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
 DR PROSITE; PS50008; PIPLC_Y_DOMAIN; 1.
 KW Calcium; Hydrolase; Lipid degradation; Metal-binding; Repeat;
 KW Transducer.
 FT CHAIN <1 1182 1-phosphatidylinositol-4,5-bisphosphate
 FT phosphodiesterase-like 4.
 FT /FTId=PRO_0000088507.
 FT DOMAIN 73 181 PH.
 FT DOMAIN 195 230 EF-hand 1.
 FT DOMAIN 231 267 EF-hand 2.
 FT DOMAIN 352 497 PI-PLC X-box.
 FT DOMAIN 652 766 PI-PLC Y-box.
 FT DOMAIN 771 878 C2.
 FT CA_BIND 208 219 Potential.
 FT ACT_SITE 367 367 By similarity.
 FT ACT_SITE 411 411 By similarity.
 FT METAL 368 368 Calcium 1 (catalytic) (By similarity).
 FT METAL 397 397 Calcium 1 (catalytic) (By similarity).
 FT METAL 399 399 Calcium 1 (catalytic) (By similarity).
 FT METAL 446 446 Calcium 1 (catalytic) (By similarity).
 FT METAL 810 810 Calcium 2 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 812 812 Calcium 2 (By similarity).
 FT METAL 836 836 Calcium 2 (By similarity).
 FT METAL 865 865 Calcium 3 (By similarity).
 FT METAL 866 866 Calcium 3 (via carbonyl oxygen) (By
 FT similarity).
 FT METAL 867 867 Calcium 3 (By similarity).
 FT BINDING 495 495 Substrate (By similarity).
 FT BINDING 497 497 Substrate (By similarity).
 FT BINDING 679 679 Substrate (By similarity).
 FT BINDING 706 706 Substrate (By similarity).
 FT NON_TER 1 1
 SQ SEQUENCE 1182 AA; 129725 MW; 4A4D4F1EBC608607 CRC64;

Query Match 91.7%; Score 5852; DB 1; Length 1182;
 Best Local Similarity 98.6%; Pred. No. 6.7e-274;
 Matches 1121; Conservative 2; Mismatches 4; Indels 10; Gaps 4;

Qy 15 PP--EDPGDPESRWLFLSANILPVVERCMGAMQEGMQMKLRGGSKGLVRFYYLDEHRS 72
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 Db 51 PPAMEEFGP-PGG---LSQD---QVERCMGAMQEGMQMKLRGGSKGLVRFYYLDEHRS 102
 Qy 73 CIRWRPSRKNEKAKISIDSIQEVSEGRQSEVFQRYPDGSFDPNCCFSIYHGSHRESLDLV 132
 |||||
 Db 103 CIRWRPSRKNEKAKISIDSIQEVSEGRQSEVFQRYPDGSFDPNCCFSIYHGSHRESLDLV 162

Qy	133	STSSSEVARTWVTGLRYLMAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIGEV LQ	192
Db	163	STSSSEVARTWVTGLRYLMAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIGEV LQ	222
Qy	193	LLHKLNVNLPQRQVKQMFREADTDDHQGT LGFEEFCAFYKMMSTRRDLYLLMLTYSNHKD	252
Db	223	LLHKLNVNLPQRQVKQMFREADTDDHQGT LGFEEFCAFYKMMSTRRDLYLLMLTYSNHKD	282
Qy	253	HLDAASLQRF LQVEQKMAGVTLESCQDI IEQFEP CPENKSKGLLGIDGFTNYTRSPAGDI	312
Db	283	HLDAASLQRF LQVEQKMAGVTLESCQDI IEQFEP CPENKSKGLLGIDGFTNYTRSPAGDI	342
Qy	313	FNPEHHHVHQDMTQPLSHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWD	372
Db	343	FNPEHHHVHQDMTQPLSHYFITSSHNTYLVGDQLMSQSRVDMYAWVLQAGCRCVEVDCWD	402
Qy	373	GPDGEPIVHHGYTLT SKILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLT	432
Db	403	GPDGEPIVHHGYTLT SKILFKDVIETINKYAFIKNEYPVILSIENHCSVIQQKKMAQYLT	462
Qy	433	DILGDKLDLSSVSSSEDATTLPS PQMLKGKILVKGKKLPANISED AEEGEVSD EDSADEID	492
Db	463	DILGDKLDLSSVSSSEDATTLPS PQMLKGKILVKGKKLPANISED AEEGEVSD EDSADEID	522
Qy	493	DDCKLLNGDASTNRKRVENTAKRKLD SLIKESKIRDCEDPNNFVS TLSPSGKLGRKSKA	552
Db	523	DDCKLLNGDASTNRKRVENTAKRKLD SLIKESKIRDCEDPNNFVS TLSPSGKLGRKSKA	582
Qy	553	EEDVESGEDAGASRRNGRLVVG SF SRRKKKGSKLKKAASVEEGDEGQDSPGGQSRGATRQ	612
Db	583	EEDVESGEDAGASRRNGRLVVG SF SRRKKKGSKLKKAASVEEGDEGQDSPGGQSRGATRQ	642
Qy	613	KKTMKLSRALSDLVKYTKSVATHD IEMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQO	672
Db	643	KKTMKLSRALSDLVKYTKSVATHD IEMEAASSWQVSSFSETKAHQILQQKPAQYLRFNQO	702
Qy	673	QLSRIYPSSYRVDSSNYPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKP	732
Db	703	QLSRIYPSSYRVDSSNYPQPFWNAGCQMVALNYQSEGRMLQLNRAKFSANGGCGYVLKP	762
Qy	733	GCMCQGVFNPNSEDPLPGQLKKQLVLR IISGQQLPKPRDSMLGDRGEIIDPFVEVEIIGL	792
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Qy	793	PVDCSREQTRVVDNNGFNPTWEETLVFMVHMPEIALVRFLVWDHDP IGRDFIGQRTLAFS	852
Db	823	PVDCSREQTRVVDNNGFNPTWEETLVFMVHMPEIALVRFLVWDHDP IGRDFIGQRTLAFS	882
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Db	883	SMMPGYRHHVYLEGME EASIFVHVA VSDISGKVKQALGLKGLFLRGPKPGSLD SHAAGRPP	942
Qy	913	ARPSVSQRILRRTASAPTKSQKPGRRGFP ELVLGTRDTGSKGVADDVVP GP GPAPAEAPA	972
Db	943	ARPSVSQRILRRTASAPTKSQKPGRRGFP ELVLGTRDTGSKGVADDVVP GP GPAPAEAPA	1002
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Db	1003	QEGPGSGSPRGKAPAAVAEKS PVRVRPPRVLDGPGPAGMAATCMKCVVGS CAGVNTGGLQ	1062
Qy	1033	RERPPSPGPASRQAAIRQQPRARADSLGAPCCGLDPHAI PGRSREAPKGP GAWRQGPGGS	1092

Db	1063	RERPPSPGPASRQAAIRQQPRARADSLGAPCCGLDPHAIPGRSREAPKGPAGAWRQGP	1122
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Seq ID NO=1

RESULT 6
AB007919
LOCUS AB007919 5450 bp mRNA linear PRI 28-JAN-2005
DEFINITION Homo sapiens mRNA for KIAA0450 protein, partial cds.
ACCESSION AB007919
VERSION AB007919.2 GI:58257651
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Seki,N., Ohira,M., Nagase,T., Ishikawa,K., Miyajima,N.,
Nakajima,D., Nomura,N. and Ohara,O.
TITLE Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain
JOURNAL DNA Res. 4 (5), 345-349 (1997)
PUBMED 9455484
REFERENCE 2 (bases 1 to 5450)
AUTHORS Ohara,O.
TITLE Direct Submission
JOURNAL Submitted (08-OCT-1997) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; Kazusa-kamatari 2-6-7, Kisarazu,
Chiba, 292-0818, Japan (E-mail:cdnainfo@kazusa.or.jp,
Tel:81-438-52-3913, Fax:81-438-52-3914)
COMMENT On Jan 27, 2005 this sequence version replaced gi:3413861.
FEATURES
source Location/Qualifiers
1. .5450
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/mol_type="mRNA"
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/note="This sequence was replaced that of hg00217 cDNA as
a representative cDNA sequence for KIAA0450."
gene 1. .5450
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CDS <1. .3551
/gene="KIAA0450"
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/product="KIAA0450 protein"
/protein_id="BAA32295.3"
/db_xref="GI:58257652"
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LVSTSSEVARTWVTGLRYLMAGISDEDSLARRQRTDQWLKQTFDEADKNGDGSLSIG
EVLQLLHKLNVNLPQRQVKQMFREADTDDHQGT LGFEFCFYKMMSTRDLVLLMLT
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CRCVEVDCWDGPDGEPIVHHGYTLTSKILFKDVIETINKYAFIKNEYPVILSIENHCS
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RMLQLNRAKFSANGGCGYVLKPGCMCQGVFNPNSEDPLPQQLKKQLVLRISGQQLPK
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ORIGIN

Query Match 72.0%; Score 3339.2; DB 5; Length 5450;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3347; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy	546	GTGGAGCGGTGCATGGGTGCCATGCAAGAGGGGATGCAGATGGTGAAGCTGCGTGGCGGC	605
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Qy	606	TCCAAGGCGCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG	665
Db	264	TCCAAGGCGCTGGTCCGCTTCTACTACCTGGACGAGCACCGCTCCTGCATCCGCTGGAGG	323
Qy	666	CCCTCACGCAAGAACGAGAAGGCCAAGATCTCCATCGACTCCATCCAGGAGGTGAGTGAG	725
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Qy	726	GGGCGGCAGTCGGAGGTCTTCAGCGCTACCTGACGGCAGCTTCGACCCCAACTGCTGC	785
Db	384	GGGCGGCAGTCGGAGGTCTTCAGCGCTACCTGACGGCAGCTTCGACCCCAACTGCTGC	443
Qy	786	TTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	845
Db	444	TTCAGCATCTACCACGGCAGCCACCGCGAGTCGCTGGACCTGGTCTCCACCAGCAGCGAG	503
Qy	846	GTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	905
Db	504	GTGGCGCGCACCTGGGTCACTGGCCTGCGCTACCTCATGGCCGGCATCAGCGACGAGGAC	563
Qy	906	AGCCTGGCTCGCCGCAGCGCACCAGGGACCAGTGGCTGAAGCAGACGTTTGACGAGGCC	965
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Db	624	GACAAGAACGGGGATGGCAGCCTGAGCATTGGCGAGGTCTGCAGCTGCTGCACAAGCTC	683
Qy	1026	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTTCAGGGAAGCGGACACGGATGAC	1085
Db	684	AACGTGAACCTGCCCCGGCAGAGGGTGAAGCAGATGTTCAGGGAAGCGGACACGGATGAC	743
Qy	1086	CACCAAGGGACGCTGGGTTTTGAAGAGTTCTGTGCCTTCTACAAGATGATGTCCACCCGC	1145
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Qy	1146	CGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCC	1205
Db	804	CGGGACCTCTACCTGCTCATGCTGACCTACAGCAACCACAAGGACCACCTGGATGCCGCC	863
Qy	1206	AGCCTGCAGCGCTTCCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGAGAGCTGC	1265
Db	864	AGCCTGCAGCGCTTCCTGCAGGTGGAGCAGAAGATGGCGGGTGTGACCCTCGAGAGCTGC	923
Qy	1266	CAGGACATCATCGAGCAGTTTGAGCCATGCCAGAAAAAAGAGTAAGGGGCTGCTGGGC	1325

Db	924		CAGGACATCATCGAGCAGTTT		GAGCCATGCCAGAAAA		CAAGAGTAAGGGGCTGCTGGGC	983
Qy	1326		ATTGATGGCTTCA		CCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCAC			1385
Db	984		ATTGATGGCTTCA		CCAACTACACCAGGAGCCCTGCTGGTGACATCTTCAACCCTGAGCAC			1043
Qy	1386		CACCATGTGCACCAGGACATGACG		CAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAC			1445
Db	1044		CACCATGTGCACCAGGACATGACG		CAGCCGCTGAGCCACTACTTCATCACCTCGTCCCAC			1103
Qy	1446		AACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGG					1505
Db	1104		AACACCTACCTCGTGGGTGACCAGCTCATGTCCCAGTCACGGGTGGACATGTATGCTTGG					1163
Qy	1506		GTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCC		GACGGGGAG			1565
Db	1164		GTCCTGCAGGCTGGCTGCCGCTGCGTGGAGGTGGACTGCTGGGATGGGCCC		GACGGGGAG			1223
Qy	1566		CCCATGTGCA		CCATGGCTACACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAA			1625
Db	1224		CCCATGTGCA		CCATGGCTACACTCTGACTTCCAAGATCCTCTTCAAAGACGTCATTGAA			1283
Qy	1626		ACCATCAACAAATATGCCTTCATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAAC					1685
Db	1284		ACCATCAACAAATATGCCTTCATCAAGAATGAGTACCCAGTGATCCTGTCCATCGAAAAC					1343
Qy	1686		CACTGCAGTGT		CATCCAGCAGAAGAAAATGGCCCAGTATCTGACTGACATCCTTGGGGAC			1745
Db	1344		CACTGCAGTGT		CATCCAGCAGAAGAAAATGGCCCAGTATCTGACTGACATCCTTGGGGAC			1403
Qy	1746		AAGCTGGACCTGT		CATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCACAGATG			1805
Db	1404		AAGCTGGACCTGT		CATCAGTGAGCAGTGAAGATGCCACCACACTCCCCTCTCCACAGATG			1463
Qy	1806		CTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCG					1865
Db	1464		CTCAAGGGCAAGATCCTCGTGAAGGGGAAGAAGCTCCCAGCCAACATCAGCGAGGATGCG					1523
Qy	1866		GAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTC					1925
Db	1524		GAGGAAGGCGAGGTGTCTGATGAGGACAGTGCTGATGAGATTGACGATGACTGCAAGCTC					1583
Qy	1926		CTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAACTG					1985
Db	1584		CTCAATGGGGATGCATCCACCAATCGAAAGCGTGTAGAAAACACTGCTAAGAGGAACTG					1643
Qy	1986		GATTCCCTCATCAAAGAGTCGAAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTC					2045
Db	1644		GATTCCCTCATCAAAGAGTCGAAGATTCGGGACTGTGAGGACCCCAACAACCTTCTCCGTC					1703
Qy	2046		TCCACACTGTCCCATCTGGAAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAG					2105
Db	1704		TCCACACTGTCCCATCTGGAAAGCTCGGACGCAAGAGCAAGGCTGAAGAGGACGTGGAG					1763
Qy	2106		TCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCTCGTCTGCGGGAAGCTTCTCC					2165
Db	1764		TCTGGGGAGGATGCCGGGGCCAGCAGACGCAATGGCCGCTCGTCTGCGGGAAGCTTCTCC					1823
Qy	2166		AGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGCCAGCGTGGAGGAGGGAGATGAG					2225

Db	1824	AGGCGCAAGAAGAAGGGCAGCAAGCTGAAGAAGGCGGCCAGCGTGGAGGAGGGAGATGAG	1883
Qy	2226	GGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAG	2285
Db	1884	GGTCAGGACTCCCCGGGAGGCCAGAGCCGAGGGGCGACCCGGCAGAAGAAGACCATGAAG	1943
Qy	2286	CTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATA	2345
Db	1944	CTGTCCCGGGCCCTCTCTGACCTGGTGAAGTACACCAAGTCCGTGGCCACCCACGACATA	2003
Qy	2346	GAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACCAG	2405
Db	2004	GAGATGGAGGCGGCGTCCAGCTGGCAGGTGTCGTCTTCAGCGAGACCAAGGCCACCAG	2063
Qy	2406	ATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCCCGCATC	2465
Db	2064	ATTCTGCAGCAGAAGCCGGCGCAGTACCTACGCTTCAACCAGCAGCAGCTCTCCCGCATC	2123
Qy	2466	TACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCC	2525
Db	2124	TACCCCTCCTCCTACCGTGTGGACTCCAGCAACTACAACCCGAGCCCTTCTGGAACGCC	2183
Qy	2526	GGTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGA	2585
Db	2184	GGTGCCAAATGGTTGCCCTGAACTACCAGTCAGAGGGGCGGATGCTGCAGCTGAACCGA	2243
Qy	2586	GCCAGTTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAG	2645
Db	2244	GCCAGTTTCAGCGCCAACGGTGGCTGCGGCTACGTACTCAAGCCTGGGTGCATGTGCCAG	2303
Qy	2646	GGCGTGTTCAAACCCCAACTCGGAGGACCCCTGCCGGGCAGCTCAAGAAGCAGCTGGTG	2705
Db	2304	GGCGTGTTCAAACCCCAACTCGGAGGACCCCTGCCGGGCAGCTCAAGAAGCAGCTGGTG	2363
Qy	2706	CTCCGGATCATCAGTGGCCAGCAGCTTCCAAGCCGCGGACTCCATGCTGGGGGACCGT	2765
Db	2364	CTCCGGATCATCAGTGGCCAGCAGCTTCCAAGCCGCGGACTCCATGCTGGGGGACCGT	2423
Qy	2766	GGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGC	2825
Db	2424	GGGGAGATCATCGACCCCTTTGTGGAGGTGGAGATCATTGGGCTCCCTGTGGACTGCAGC	2483
Qy	2826	AGGGAGCAGACCCGCGTGGTGGACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTG	2885
Db	2484	AGGGAGCAGACCCGCGTGGTGGACGACAACGGGTTCAACCCACCTGGGAGGAGACCCTG	2543
Qy	2886	GTTTTTCATGGTGCACATGCCGAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGAT	2945
Db	2544	GTTTTTCATGGTGCACATGCCGAGATCGCGCTGGTCCGCTTCCTCGTCTGGGACCACGAT	2603
Qy	2946	CCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGC	3005
Db	2604	CCCATCGGGCGTGACTTCATTGGCCAGAGGACGCTGGCCTTCAGCAGCATGATGCCAGGC	2663
Qy	3006	TACAGACACGTGTACCTAGAAGGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTC	3065
Db	2664	TACAGACACGTGTACCTAGAAGGGATGGAAGAGGCCTCCATCTTCGTGCATGTGGCTGTC	2723
Qy	3066	AGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGC	3125
Db	2724	AGTGACATCAGCGGTAAGGTCAAGCAGGCTCTGGGCCTAAAAGGCCTCTTCCTCCGAGGC	2783

Qy	3126	CCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTT	3185
Db	2784	CCAAAGCCCGGCTCGCTGGACAGTCATGCTGCTGGGCGGCCCCCGGCCCGGCCCTCCGTT	2843
Qy	3186	AGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGC	3245
Db	2844	AGCCAGCGGATCCTGCGGCGCACGGCCAGCGCCCCGACCAAGAGCCAGAAGCCGGGCCGC	2903
Qy	3246	AGGGGCTTCCCGAGCTGGTCCTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGAC	3305
Db	2904	AGGGGCTTCCCGAGCTGGTCCTGGGTACACGGGACACAGGCTCCAAGGGGTGGCAGAC	2963
Qy	3306	GATGTGGTGCCCCCGGGCCCGGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCCGGC	3365
Db	2964	GATGTGGTGCCCCCGGGCCCGGACCTGCTCCGGAAGCCCCAGCCAGGAGGGGCCCGGC	3023
Qy	3366	AGCGGCAGCCCCGAGGTAAGGCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTG	3425
Db	3024	AGCGGCAGCCCCGAGGTAAGGCGCCAGCTGCGGTGGCAGAGAAGAGCCCTGTGCGAGTG	3083
Qy	3426	CGGCCCCCGCGTGTCTTGACGGCCCCGGGCTGCTGGGATGGCCGCCACATGCATGAAG	3485
Db	3084	CGGCCCCCGCGTGTCTTGACGGCCCCGGGCTGCTGGGATGGCCGCCACATGCATGAAG	3143
Qy	3486	TGTGTGGTGGGATCCTGCGCCGGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCC	3545
Db	3144	TGTGTGGTGGGATCCTGCGCCGGCGTGAACACCGGGGGCCTGCAGAGGGAGCGGCCACCC	3203
Qy	3546	AGCCCGGGGCTGCAAGCAGGCAGGCAGCCATTCCGCAGCAGCCCCGGGCCCGGGCTGAC	3605
Db	3204	AGCCCGGGGCTGCAAGCAGGCAGGCAGCCATTCCGCAGCAGCCCCGGGCCCGGGCTGAC	3263
Qy	3606	TCACTGGGGGCCCCCTGCTGTGGCCTGGACCTCACGCTATCCCGGGGAGAAGCAGAGAG	3665
Db	3264	TCACTGGGGGCCCCCTGCTGTGGCCTGGACCTCACGCTATCCCGGGGAGAAGCAGAGAG	3323
Qy	3666	GCCCCAAGGGTCCTGGGGCCTGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCCTCG	3725
Db	3324	GCCCCAAGGGTCCTGGGGCCTGGAGGCAGGGTCCAGGCGGTAGCGGCTCCATGTCCTCG	3383
Qy	3726	GACTCCAGCAGCCAGACAGCCCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGT	3785
Db	3384	GACTCCAGCAGCCAGACAGCCCGGGCATCCCCGAAAGGTCCCCCGCTGGCCTGAGGGT	3443
Qy	3786	GCCTGCAGGCAACCGGGGGCCCTGCAGGGAGAGATGAGTGCCTTGTTTGCTCAAAAGCTG	3845
Db	3444	GCCTGCAGGCAACCGGGGGCCCTGCAGGGAGAGATGAGTGCCTTGTTTGCTCAAAAGCTG	3503
Qy	3846	GAGGAGATCAGGAGTAAATCCCCCATGTTCTCCGCCGGTAAGCCCCCTTGCCCTGCGTG	3905
Db	3504	GAGGAGATCAGGAGTAAATCCCCCATGTTCTCCGCCGTAGGAACTGAGAGCGGCGAGTG	3563